

05/10  
6426

OIKE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/084,971

DATE: 05/01/2002

TIME: 10:58:34

Input Set : N:\Crf3\RULE60\10084971.raw

Output Set: N:\CRF3\05012002\J084971.raw

1 <110> APPLICANT: Human Genome Sciences, Inc.  
 2 <120> TITLE OF INVENTION: Neutrokin-alpha Binding Proteins and Methods Based Thereon  
 3 <130> FILE REFERENCE: PF524PCT  
 4 <140> CURRENT APPLICATION NUMBER: 10/084,971  
 5 <141> CURRENT FILING DATE: 2002-03-01  
 7 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/533,822  
 W--> 8 <151> PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-24  
 10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/126,599  
 W--> 11 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-26  
 12 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/188,208  
 W--> 13 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-10  
 14 <160> NUMBER OF SEQ ID NOS: 5  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 882  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Homo sapiens  
 21 <220> FEATURE:  
 22 <221> NAME/KEY: CDS  
 23 <222> LOCATION: (1)..(882)  
 24 <400> SEQUENCE: 1

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26	Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp	
27	1 5 10 15	
28	cag gag gag cgc ttt cca cag ggc ctg tgg acg ggg gtg gct atg aga	96
29	Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg	
30	20 25 30	
31	tcc tgc ccc gaa gag cag tac tgg gat cct ctg ctg ggt acc tgc atg	144
32	Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met	
33	35 40 45	
34	tcc tgc aaa acc att tgc aac cat cag agc cag cgc acc tgt gca gcc	192
35	Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala	
36	50 55 60	
37	ttc tgc agg tca ctc agc tgc cgc aag gag caa ggc aag ttc tat gac	240
38	Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp	
39	65 70 75 80	
40	cat ctc ctg agg gac tgc atc agc tgt gcc tcc atc tgt gga cag cac	288
41	His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His	
42	85 90 95	
43	cct aag caa tgt gca tac ttc tgt gag aac aag ctc agg agc cca gtg	336
44	Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val	
45	100 105 110	
46	aac ctt cca cca gag ctc agg aga cag cgg agt gga gaa gtt gaa aac	384

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Input Set : N:\Crif3\RULE60\10084971.raw

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47   Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
48       115                               120                               125
49   aat tca gac aac tcg gga agg tac caa gga ttg gag cac aga ggc tca   432
50   Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
51       130                               135                               140
52   gaa gca agt cca gct ctc ccg ggg ctg aag ctg agt gca gat cag gtg   480
53   Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
54       145                               150                               155
55   gcc ctg gtc tac agc acg ctg ggg ctc tgc ctg tgt gcc gtc ctc tgc   528
56   Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
57       165                               170                               175
58   tgc ttc ctg gtg gcg gtg gcc tgc ttc ctc aag aag agg ggg gat ccc   576
59   Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
60       180                               185                               190
61   tgc tcc tgc cag ccc cgc tca agg ccc cgt caa agt ccg gcc aag tct   624
62   Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
63       195                               200                               205
64   tcc cag gat cac gcg atg gaa gcc ggc agc cct gtg agc aca tcc ccc   672
65   Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
66       210                               215                               220
67   gag cca gtg gag acc tgc agc ttc tgc ttc cct gag tgc agg gcg ccc   720
68   Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
69       225                               230                               235
70   acg cag gag agc gca gtc acg cct ggg acc ccc gac ccc act tgt gct   768
71   Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
72       245                               250                               255
73   gga agg tgg ggg tgc cac acc agg acc aca gtc ctg cag cct tgc cca   816
74   Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
75       260                               265                               270
76   cac atc cca gac agt ggc ctt ggc att gtg tgt gtg cct gcc cag gag   864
77   His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
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80   Gly Gly Pro Gly Ala   882
81       290
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84 <211> LENGTH: 293
85 <212> TYPE: PRT
86 <213> ORGANISM: Homo sapiens
87 <400> SEQUENCE: 2
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91       20                               25                               30
92   Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met
93       35                               40                               45
94   Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala
95       50                               55                               60
96   Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp

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97      65      70      75      80
98 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His
99      85      90      95
100 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val
101      100      105      110
102 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn
103      115      120      125
104 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser
105      130      135      140
106 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val
107      145      150      155      160
108 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys
109      165      170      175
110 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro
111      180      185      190
112 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser
113      195      200      205
114 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro
115      210      215      220
116 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro
117      225      230      235      240
118 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala
119      245      250      255
120 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro
121      260      265      270
122 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu
123      275      280      285
124 Gly Gly Pro Gly Ala
125      290
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128 <211> LENGTH: 733
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130 <213> ORGANISM: Homo sapiens
131 <400> SEQUENCE: 3
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133 aattcgaggg tgcaccgtca gtcttcctct tcccccaaaa acccaaggac accctcatga 120
134 tctcccgac tcttgaggtc acatgcgtgg tgggtggacgt aagccacgaa gacctgagg 180
135 tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
136 aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
137 ggctgaatgg caaggagtac aagtgcgaagg totccaacaa agccctccca acccccatcg 360
138 agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
139 catcccgga tgagctgacc aagaaccagg tcagcctgac ctgcctgggc aaaggcttct 480
140 atccaagcga catgcgcgtg gagtgaggaga gcaatgggca gccggagaac aactacaaga 540
141 ccacgcctcc cgtgctggac tccgacggct ccttcttct ctacagcaag ctaccgtgg 600
142 acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcac gaggctctgc 660
143 acaaccacta cagcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
144 gactctagag gat
146 <210> SEQ ID NO: 4
147 <211> LENGTH: 9

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Output Set: N:\CRF3\05012002\J084971.raw

148 <212> TYPE: PRT  
149 <213> ORGANISM: Homo sapiens  
150 <220> FEATURE:  
151 <221> NAME/KEY: SITE  
152 <222> LOCATION: (1)..(5)  
153 <223> OTHER INFORMATION: Xaa equal any amino acid  
154 <220> FEATURE:  
155 <221> NAME/KEY: SITE  
156 <222> LOCATION: (9)  
157 <223> OTHER INFORMATION: Xaa equal any amino acid  
158 <400> SEQUENCE: 4  
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160 1 5  
162 <210> SEQ ID NO: 5  
163 <211> LENGTH: 9  
164 <212> TYPE: PRT  
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166 <220> FEATURE:  
167 <221> NAME/KEY: SITE  
168 <222> LOCATION: (3)  
169 <223> OTHER INFORMATION: Xaa equal any amino acid  
170 <400> SEQUENCE: 5  
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172 1 5

RAW SEQUENCE LISTING ERROR SUMMARY  
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Input Set : N:\Crf3\RULE60\10084971.raw  
Output Set: N:\CRF3\05012002\J084971.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 1,2,3,4,5,9  
Seq#:5; Xaa Pos. 3

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 2

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10084971.raw

Output Set: N:\CRF3\05012002\J084971.raw

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L:11 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:13 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD  
L:159 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:0  
L:171 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0